SEARCH REQUEST FORM

1 x7

	Requestor's Name: S UNGAR Date: 7/6/98 P	Serial Number: <u>-0</u> hone: <u>35-218/</u>	& /& 4&, 434 Art Unit: _/& 42
	Search Topic: Please write a detailed statement of search topi terms that may have a special meaning. Give explease attach a copy of the sequence. You may	camples or relevent citations, authors, keys include a copy of the broadest and/or most	words, etc., if known. For sequences,
	SEQ ID #	₹	™ com a Salamasir
	Please C. 2014	SEQID#1 to Rev	use Transculed
	Pluse Congrais	Seg ID# 1 To 1	were transceled
	Sé	QID#3	9 JU - 7 M
		Thoules June 8	\$ 37
• 53			
•		STAFF USE ONLY	
;	Date completed: 7-(0-98	Search Site	Vendors
-	Searcher:	STIC / CM-1	IG- FG STN
	Elapsed time:	Pre-S	STN Dialog
1	CPU time:	Type of Search	APS
	Total time: / /	N.A. Sequence	Geninfo
	Number of Searches:	A.A. Sequence	SDC
:	Number of Databases:	Structure Bibliographic	DARC/Questel Other
	1	Dionographic	Other

PTO-1590 (9-90)

Sequence Name

Description

Length Score

Opt. Score

Sig. Frame

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SCORE 0
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0 0 ∨
0 0 ∨
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                                                                                                        Gap penalty
Gap size penalty
Cutoff score
                                                 Scores:
                                                                                                                                         Similarity matrix Mismatch penalty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query sequence being compared:US-08-848-439-1 (1-2027)
Number of sequences searched:
2
Number of scores above cutoff:
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Results file us-08-848-439-1.res made by spencer on Fri 10 Jul 98 15:04:54-PDT
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                                                                                              Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Results of the initial comparison of US-08-848-439-1 (1-2027) with: File : translate.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IntelliGenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Past Pairwise Comparison of Sequences
5.4
                                                                                                                                                                                                                             158
CPU
00:00:00.00
                                                                                                                                                      Unitary
                                   Mean
682
                                                                                                                                                                                                                             238
                                                                                                                    1.00
0.33
                                                                       SEARCH STATISTICS
                                                                                                                                                                             PARAMETERS
                                                                                                                             K-tuple
Joining penalty
Window size
                                    Median
653
                                                                                                                                                                                                                 3961
                                   Standard Deviation 43.13
Total Elapsed 00:00:00:00.00.
                                                                                                                                30
                                                                                                                                                                                                                           713
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Number of residues:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                          Times:
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Gaps

The scores below are sorted by initial Significance is calculated based on in lal score. initial score.

A 100% identical sequence to the query sequence was not found

The list of best scores is:

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Initial Score Residue Identity - Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. US 108 3448 439 71 41 42027) 7 Application US 7088484397
                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein

Reverse Translation from the peptide US-08-848-439-2.

Note: the original peptide US-08-848-439-2 contained at least one of the residues Arg, Ile, Leu, or Ser. The nucleic acid sequence thus contains ambiguous bases which may translate into amino acids other than the original amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08848439 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENCTH: 295 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. US-08-848-439-2 Sequence 2, Application 2. US-08-848-439-3 Sequence 3, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, STEVEN R.
REGISTRATION NUMBER: 32,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
                                                                                             AYTTYWSNTAYAARMGNWSNAAYTGYAARCCNATNCCNGCNAAYYTNCARYTNTGYCAYGGNATNGARTAYC 100 110 150 160 .
                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: RACIE, LISA
TITLE OF INVENTION: HUMAN SDF-5 PROTEIN AND COMPOSITIONS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MA
COUNTRY: US
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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linear
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                                                                                                                                                                                                                                                                                       713
58%
0
                                                                                                                                                                                                                                                                                  Optimized Score - 734
Matches - 734
Conservative Substitutions
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Mismatches
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Sequence 3, Application US/08848439
GENERAL INFORMATION:
APPLICANT: LAVALLE, EDWARD
APPLICANT: RACIE, LISA
TITLE OF INVENTION: HUMAN SDF-5
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                              .F05-08-848-439-1-(112027) ** TROUBLE CONTROL OF TRANSPORT OF TRANSPOR
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320 330 340 350 360 370 380
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      HUMAN SDF-5 PROTEIN: 3
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INFORMATION: (617) 498-8260
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Residue
                                                                                                                                                                                                                                                                                                                                                                                                                                         Initial Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein

Reverse Translation from the peptide US-08-848-439-3.

Reverse Translation from the peptide US-08-848-439-3 contained at least one of the residues Arg, Ile, Leu, or Ser: The nucleic acid sequence thus contains ambiguous bases which may translate into amino acother than the original amino acids.
                                                                                                                                                                                                       ZIP: 02140
COMPUTER READABLE FORM:
EDIUM TYPE: Floppy disk
                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE,
STREET: 87 CAMBRIDGEPARK DRIVE
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, STEVEN R.
REGISTRATION UNDER: 32,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 87 CAMBR
CITY: CAMBRIDGE
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                             Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                   652
59%
0
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                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                              883
883
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1130 1140 1150 1160 1170 1180 1190 AGCTGCAGTGCTAGTCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTG APTINCARTGY B20 X	1060 1070 1080 1090 1100 1110 1110 1120 1200 1090 109	990 1000 1010 1020 1030 1040 1050 AGTGCACCTGTGAGGAGATGAACGACACCACCCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGC	920 930 940 950 960 970 980 CCATTTACAAGCTGAACGGTGTGTCCCGAAAGGGACCTGAAGAAATCGGTGCTGTGGCTCAAAGACAGCTTGC	850 860 870 880 990 900 910 TGAAAATAAAGTGAAGGAGATAACCTACATCAACCGAGAATCATCCTGGAGACCAAGAGCAAGAG	770 780 790 800 810 820 830 840 GTGAAGCCTGCAAAAAATGAATGATGACAACGACATAATGGAAACGCTTTGTAAAAATGATTTTGCAC	700 710 720 730 740 750 760 760 760 760 760 760 760 760 760 76	320 330 340 350 360 370
CTG	1120 CCGCAGCATCCGCA NMGNWSNATNMGNA 810	1050 ACAGGGTGGGGAGC RCARGGNGGNGARY 30 740	980 CAAAGACAGCTTGC 1 NAARGAYWSNYTNC 660 670	910 GACCAAGAGCAAGA 	840 AAATGATTTTGCAC RAAYGAYTTYGCNY	760 AGCTCCAAAGGTAT 	70 . 380
				•			